

00969180-040909

Sub
11

<130> P148946

<150> JP 10/099619

<151> 1998-04-10

<160> 14

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<211> 477

<212> PRT

<213> Rattus norvegicus

<400> 1

56

00289180 040999

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Thr	His	Gly	Ser	Met	Leu	Leu	Gly	Leu	Leu	Leu	Gly	Ala	Gly	Gln	Thr
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Pro	Gln	Pro	Asn	Ser	Ser	Leu	Ile	Arg	Gln	Ala	Arg	Ala	Glu	Arg	Trp
	210					215					220				
Ser	Gln	Trp	Ser	Leu	Arg	Gly	Gly	Leu	Glu	Met	Leu	Pro	Gln	Ala	Leu
225					230					235					240
His	Asn	Tyr	Leu	Thr	Ser	Lys	Gly	Val	Thr	Ile	Leu	Ser	Gly	Gln	Pro
				245					250					255	
Ala	Cys	Gly	Leu	Ser	Leu	Gln	Pro	Glu	Gly	His	Trp	Lys	Val	Ser	Leu
			260					265					270		
Gly	Asp	Ser	Ser	Leu	Glu	Ala	Asp	His	Ile	Ile	Ser	Thr	Ile	Pro	Ala
		275					280					285			
Ser	Val	Leu	Ser	Lys	Leu	Leu	Pro	Ala	Glu	Ala	Ala	Pro	Leu	Ala	His
	290					295					300				
Ile	Leu	Ser	Thr	Ile	Gln	Ala	Val	Ser	Val	Ala	Val	Val	Asn	Leu	Gln
305					310					315					320
Tyr	Lys	Gly	Ala	Cys	Leu	Pro	Val	Gln	Gly	Phe	Gly	His	Leu	Val	Pro
				325					330					335	
Ser	Ser	Glu	Asp	Pro	Thr	Val	Leu	Gly	Ile	Val	Tyr	Asp	Ser	Val	Ala
			340					345					350		
Phe	Pro	Glu	Gln	Asp	Gly	Asn	Pro	Pro	Gly	Leu	Arg	Leu	Thr	Val	Met
		355					360					365			
Leu	Gly	Gly	Tyr	Trp	Leu	Gln	Lys	Leu	Lys	Ala	Asn	Gly	His	Glu	Leu
	370					375					380				
Ser	Pro	Glu	Leu	Phe	Gln	Arg	Ala	Ala	Gln	Glu	Ala	Ala	Ala	Thr	Gln
385					390					395					400
Leu	Gly	Leu	Lys	Glu	Gln	Pro	Ser	His	Cys	Leu	Val	His	Leu	His	Lys
				405					410					415	
Asn	Cys	Ile	Pro	Gln	Tyr	Thr	Leu	Gly	His	Trp	Gln	Lys	Leu	Asp	Ser
			420					425					430		
Ala	Leu	Gln	Phe	Leu	Thr	Ala	Gln	Arg	Leu	Pro	Leu	Thr	Leu	Ala	Gly
		435					440					445			
Ala	Ser	Tyr	Glu	Gly	Val	Ala	Val	Asn	Asp	Cys	Ile	Glu	Ser	Gly	Arg
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<211> 1638

<213> Rattus norvegicus

$\langle 222 \rangle$ (143)...(1576)

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CGACTTTCCC CCAGGCCCTTA CG ATG GCC CGG ACT GTG ATA GTG CTT GGC GGA	172
Met Ala Arg Thr Val Ile Val Leu Gly Gly	
1 5 10	
GGT ATC AGC GGA TTG GCC GCA AGT TAT CAT CTG ACC CGA AGC CCC AGT	220
Gly Ile Ser Gly Leu Ala Ala Ser Tyr His Leu Thr Arg Ser Pro Ser	
15 20 25	
CCT CCT AAG GTG ATC TTA GTG GAG GGC AGC AAA CGT TTG GGA GGC TGG	268
Pro Pro Lys Val Ile Leu Val Glu Gly Ser Lys Arg Leu Gly Gly Trp	
30 35 40	
ATC CGT TCA GTC CGA GGA TCA GAT GGT GCG ATC TTT GAA CTT GGA CCT	316
Ile Arg Ser Val Arg Gly Ser Asp Gly Ala Ile Phe Glu Leu Gly Pro	
45 50 55	
CGA GGA ATT AGG CCG GCT GGA GCC CTG GGA GCC CGG ACC CTG CTC CTG	364
Arg Gly Ile Arg Pro Ala Gly Ala Leu Gly Ala Arg Thr Leu Leu Leu	
60 65 70	
GTT TCT GAA CTT GGC TTG GAA TCC GAA GTC TTG CCT GTC CGA GGG GAT	412
Val Ser Glu Leu Gly Leu Glu Ser Glu Val Leu Pro Val Arg Gly Asp	
75 80 85 90	
CAT CCA GCT GCC CAG AAC CGG TTC CTG TAT GTA GGC GGT GCC CTG CAC	460
His Pro Ala Ala Gln Asn Arg Phe Leu Tyr Val Gly Gly Ala Leu His	
95 100 105	
CCC CTA CCC TCT GGC CTC AGG GGG CTA CTT CGT CCT TCA CCC CCC TTC	508
Pro Leu Pro Ser Gly Leu Arg Gly Leu Leu Arg Pro Ser Pro Pro Phe	
110 115 120	
TCA AAA CCT CTA TTT TGG GCT GGA CTG AGG GAG TTG ACG AAG CCC AGG	556
Ser Lys Pro Leu Phe Trp Ala Gly Leu Arg Glu Leu Thr Lys Pro Arg	
125 130 135	
GGC AAA GAG CCT GAT GAG ACT GTG CAC AGT TTT GCC CAG CGC CGC CTT	604
Gly Lys Glu Pro Asp Glu Thr Val His Ser Phe Ala Gln Arg Arg Leu	
140 145 150	
GGA CCT GAG GTG GCG TCT CTG GCT ATG GAC AGC CTT TGC AGA GGA GTG	652

Gly 155	Pro	Glu	Val	Ala	Ser 160	Leu	Ala	Met	Asp	Ser	Leu	Cys	Arg	Gly	Val 170	
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Phe	Ala	Gly	Asn	Ser	Gln	Glu	Leu	Ser	Ile	Arg	Ser	Cys	Phe	Pro	Ser	
				175					180					185		
CTC	TTC	CAA	GCT	GAA	CAA	ACC	CAC	GGG	TCC	ATG	TTA	CTG	GGG	CTG	CTG	748
Leu	Phe	Gln	Ala	Glu	Gln	Thr	His	Gly	Ser	Met	Leu	Leu	Gly	Leu	Leu	
			190					195					200			
CTG	GGG	GCA	GGG	CAA	ACT	CCA	CAG	CCC	AAT	TCC	TCA	TTA	ATT	CGT	CAG	796
Leu	Gly	Ala	Gly	Gln	Thr	Pro	Gln	Pro	Asn	Ser	Ser	Leu	Ile	Arg	Gln	
	205						210					215				
GCC	CGC	GCT	GAG	CGA	TGG	AGT	CAG	TGG	TCA	CTC	CGT	GGA	GGG	CTG	GAG	844
Ala	Arg	Ala	Glu	Arg	Trp	Ser	Gln	Trp	Ser	Leu	Arg	Gly	Gly	Leu	Glu	
	220					225				230						
ATG	TTG	CCC	CAG	GCC	CTT	CAT	AAC	TAC	CTA	ACA	AGT	AAA	GGG	GTC	ACT	892
Met	Leu	Pro	Gln	Ala	Leu	His	Asn	Tyr	Leu	Thr	Ser	Lys	Gly	Val	Thr	
235				240					245					250		
ATC	CTC	AGT	GGT	CAG	CCA	GCC	TGC	GGG	CTC	AGC	CTT	CAG	CCA	GAA	GGG	940
Ile	Leu	Ser	Gly	Gln	Pro	Ala	Cys	Gly	Leu	Ser	Leu	Gln	Pro	Glu	Gly	
			255					260					265			
CAC	TGG	AAG	GTG	TCT	CTA	GGG	GAC	AGC	AGT	CTG	GAG	GCT	GAC	CAC	ATT	988
His	Trp	Lys	Val	Ser	Leu	Gly	Asp	Ser	Ser	Leu	Glu	Ala	Asp	His	Ile	
			270					275					280			
ATA	AGC	ACC	ATT	CCA	GCT	TCA	GTG	CTC	AGC	AAG	CTG	CTC	CCT	GCC	GAG	1036
Ile	Ser	Thr	Ile	Pro	Ala	Ser	Val	Leu	Ser	Lys	Leu	Leu	Pro	Ala	Glu	
	285						290					295				
GCT	GCA	CCT	CTG	GCT	CAC	ATC	CTG	AGT	ACC	ATC	CAA	GCT	GTG	TCT	GTG	1084
Ala	Ala	Pro	Leu	Ala	His	Ile	Leu	Ser	Thr	Ile	Gln	Ala	Val	Ser	Val	
	300					305					310					
GCC	GTG	GTG	AAT	CTG	CAG	TAC	AAA	GGA	GCT	TGT	CTG	CCT	GTG	CAG	GGA	1132
Ala	Val	Val	Asn	Leu	Gln	Tyr	Lys	Gly	Ala	Cys	Leu	Pro	Val	Gln	Gly	
315				320				325					330			
TTT	GGA	CAT	CTG	GTG	CCA	TCC	TCA	GAA	GAC	CCG	ACC	GTC	CTG	GGA	ATC	1180
Phe	Gly	His	Leu	Val	Pro	Ser	Ser	Glu	Asp	Pro	Thr	Val	Leu	Gly	Ile	
			335					340					345			
GTG	TAT	GAC	TCG	GTT	GCT	TTT	CCT	GAG	CAG	GAT	GGG	AAC	CCC	CCA	GGC	1228
Val	Tyr	Asp	Ser	Val	Ala	Phe	Pro	Glu	Gln	Asp	Gly	Asn	Pro	Pro	Gly	
			350					355					360			
CTC	AGA	CTG	ACT	GTG	ATG	TTG	GGA	GGT	TAC	TGG	TTA	CAG	AAG	CTG	AAA	1276
Leu	Arg	Leu	Thr	Val	Met	Leu	Gly	Gly	Tyr	Trp	Leu	Gln	Lys	Leu	Lys	
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GCC AAT GGC CAT GAA TTG TCT CCA GAG CTA TTC CAA CGA GCA GCA CAG 1324
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 380 385 390
 GAA GCG GCT GCC ACA CAG TTA GGA CTG AAA GAG CAA CCA AGC CAT TGC 1372
 Glu Ala Ala Ala Thr Gln Leu Gly Leu Lys Glu Gln Pro Ser His Cys
 395 400 405 410
 TTG GTC CAT CTA CAC AAA AAC TGT ATC CCT CAG TAT ACA CTA GGC CAC 1420
 Leu Val His Leu His Lys Asn Cys Ile Pro Gln Tyr Thr Leu Gly His
 415 420 425
 TGG CAA AAA CTA GAC TCA GCT CTG CAA TTC CTG ACG GCC CAG AGG TTG 1468
 Trp Gln Lys Leu Asp Ser Ala Leu Gln Phe Leu Thr Ala Gln Arg Leu
 430 435 440
 CCC CTG ACT TTG GCT GGG GCC TCC TAT GAG GGG GTA GCT GTC AAT GAC 1516
 Pro Leu Thr Leu Ala Gly Ala Ser Tyr Glu Gly Val Ala Val Asn Asp
 445 450 455
 TGT ATA GAG AGT GGG CGC CAG GCA GCA ATT GCT GTC CTG GGC ACA GAA 1564
 Cys Ile Glu Ser Gly Arg Gln Ala Ala Ile Ala Val Leu Gly Thr Glu
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 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer used for amplifying a DNA fragment
 containing a partial nucleotide sequence of a rat-derived PPO gene

<400> 3

TTTGCAGAGG AGTGTTTGCT GGCAACAG 28

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial Sequence

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<223> Designed oligonucleotide primer used for amplifying a DNA fragment containing a partial nucleotide sequence of a rat-derived PPO gene

<400> 4

AGCCGCTTCC TGTGCTGCTC GTTGAATA 29

<210> 5

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer used for constructing a vector expressing a rat-derived PPO gene in *Escherichia coli*

<400> 5

AGGCCTTACC GCGGCCCGGA CTGTG 25

<210> 6

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer used for constructing a vector expressing a rat-derived PPO gene in *Escherichia coli*

<400> 6

TAGGAGAGCC CGGGTCAGAT GTTCG 25

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide primer used for constructing a rat-derived PPO gene expression vector for direct introduction and a rat-derived PPO expression vector for indirect introduction

<400> 7

ATGGCCCGGA CTGTGATAGT GCTTG 25

<210> 8

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide primer used for constructing a rat-derived PPO gene expression vector for direct introduction and a rat-derived PPO expression vector for indirect introduction

<400> 8

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<210> 9

<211> 563

<212> PRT

<213> *Chlamydomonas reinhardtii* CC-407

<400> 9

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Ser	Gln	Ile	Arg	Ser	Ala	Ala	His	Val	Ser	Ala	Lys	Val	Ala	Pro	Arg
			20					25					30		
Pro	Thr	Pro	Phe	Ser	Val	Ala	Ser	Pro	Ala	Thr	Ala	Ala	Ser	Pro	Ala
		35					40					45			
Thr	Ala	Ala	Ala	Arg	Arg	Thr	Leu	His	Arg	Thr	Ala	Ala	Ala	Ala	Thr
	50					55				60					
Gly	Ala	Pro	Thr	Ala	Ser	Gly	Ala	Gly	Val	Ala	Lys	Thr	Leu	Asp	Asn
65				70					75				80		
Val	Tyr	Asp	Val	Ile	Val	Val	Gly	Gly	Gly	Leu	Ser	Gly	Leu	Val	Thr
			85					90					95		
Gly	Gln	Ala	Leu	Ala	Ala	Gln	His	Lys	Ile	Gln	Asn	Phe	Leu	Val	Thr
		100						105					110		
Glu	Ala	Arg	Glu	Arg	Val	Gly	Gly	Asn	Ile	Thr	Ser	Met	Ser	Gly	Asp
	115					120						125			
Gly	Tyr	Val	Trp	Glu	Glu	Gly	Pro	Asn	Ser	Phe	Gln	Pro	Asn	Asp	Ser

130					135					140						
Met	Leu	Gln	Ile	Ala	Val	Asp	Ser	Gly	Cys	Glu	Lys	Asp	Leu	Val	Phe	
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Gly	Asp	Pro	Thr	Ala	Pro	Arg	Phe	Val	Trp	Trp	Glu	Gly	Lys	Leu	Arg	
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180					185					190						
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195					200					205						
Ala	Met	Pro	Ser	Phe	Glu	Glu	Ser	Val	Glu	Gln	Phe	Ile	Arg	Arg	Asn	
210					215					220						
Leu	Gly	Asp	Glu	Val	Phe	Phe	Arg	Leu	Ile	Glu	Pro	Phe	Cys	Ser	Gly	
225					230					235					240	
Val	Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	Asn	
245					250					255						
Arg	Ile	Trp	Ile	Leu	Glu	Lys	Asn	Gly	Gly	Ser	Leu	Val	Gly	Gly	Ala	
260					265					270						
Ile	Lys	Leu	Phe	Gln	Glu	Arg	Gln	Ser	Asn	Pro	Ala	Pro	Pro	Arg	Asp	
275					280					285						
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290					295					300						
Lys	Gly	Leu	Lys	Met	Leu	Pro	Asp	Ala	Ile	Glu	Arg	Asn	Ile	Pro	Asp	
305					310					315					320	
Lys	Ile	Arg	Val	Asn	Trp	Lys	Leu	Val	Ser	Leu	Gly	Arg	Glu	Ala	Asp	
325					330					335						
Gly	Arg	Tyr	Gly	Leu	Val	Tyr	Asp	Thr	Pro	Glu	Gly	Arg	Val	Lys	Val	
340					345					350						
Phe	Ala	Arg	Ala	Val	Ala	Leu	Thr	Ala	Pro	Ser	Tyr	Val	Val	Ala	Asp	
355					360					365						
Leu	Val	Lys	Glu	Gln	Ala	Pro	Ala	Ala	Ala	Glu	Ala	Leu	Gly	Ser	Phe	
370					375					380						
Asp	Tyr	Pro	Pro	Val	Gly	Ala	Val	Thr	Leu	Ser	Tyr	Pro	Leu	Ser	Ala	
385					390					395					400	
Val	Arg	Glu	Glu	Arg	Lys	Ala	Ser	Asp	Gly	Ser	Val	Pro	Gly	Phe	Gly	
405					410					415						
Gln	Leu	His	Pro	Arg	Thr	Gln	Gly	Ile	Thr	Thr	Leu	Gly	Thr	Ile	Tyr	
420					425					430						
Ser	Ser	Ser	Leu	Phe	Pro	Gly	Arg	Ala	Pro	Glu	Gly	His	Met	Leu	Leu	
435					440					445						
Leu	Asn	Tyr	Ile	Gly	Gly	Thr	Thr	Asn	Arg	Gly	Ile	Val	Asn	Gln	Thr	
450					455					460						

[illegible]

$\langle 210 \rangle$ 10
 $\langle 211 \rangle$ 1838
 $\langle 212 \rangle$ DNA
 $\langle 213 \rangle$ *Chlamydomonas reinhardtii* CC-407

 $\langle 400 \rangle$ 10

Asn	Val	Tyr	Asp	Val	Ile	Val	Val	Gly	Gly	Gly	Leu	Ser	Gly	Leu	Val	
80					85					90					95	
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Thr	Gly	Gln	Ala	Leu	Ala	Ala	Gln	His	Lys	Ile	Gln	Asn	Phe	Leu	Val	
				100					105					110		
ACG	GAG	GCT	CGC	GAG	GCG	GTC	GGC	GGC	AAC	ATT	ACG	TCC	ATG	TCG	GGC	382
Thr	Glu	Ala	Arg	Glu	Arg	Val	Gly	Gly	Asn	Ile	Thr	Ser	Met	Ser	Gly	
			115					120					125			
GAT	GGC	TAC	GTG	TGG	GAG	GAG	GGC	CCG	AAC	AGC	TTC	CAG	CCC	AAC	GAT	430
Asp	Gly	Tyr	Val	Trp	Glu	Glu	Gly	Pro	Asn	Ser	Phe	Gln	Pro	Asn	Asp	
		130					135					140				
AGC	ATG	CTG	CAG	ATT	GCG	GTG	GAC	TCT	GGC	TGC	GAG	AAG	GAC	CTT	GTG	478
Ser	Met	Leu	Gln	Ile	Ala	Val	Asp	Ser	Gly	Cys	Glu	Lys	Asp	Leu	Val	
	145					150				155						
TTC	GGT	GAC	CCC	ACG	GCT	CCC	CGC	TTC	GTG	TGG	TGG	GAG	GGC	AAG	CTG	526
Phe	Gly	Asp	Pro	Thr	Ala	Pro	Arg	Phe	Val	Trp	Trp	Glu	Gly	Lys	Leu	
160					165				170					175		
CGC	CCC	GTG	CCC	TCG	GGC	CTG	GAC	GCC	TTC	ACC	TTC	GAC	CTC	ATG	TCC	574
Arg	Pro	Val	Pro	Ser	Gly	Leu	Asp	Ala	Phe	Thr	Phe	Asp	Leu	Met	Ser	
				180					185					190		
ATC	CCC	GGC	AAG	ATC	CGC	GCC	GGG	CTG	GGC	GCC	ATC	GGC	CTC	ATC	AAC	622
Ile	Pro	Gly	Lys	Ile	Arg	Ala	Gly	Leu	Gly	Ala	Ile	Gly	Leu	Ile	Asn	
		195					200					205				
GGA	GCC	ATG	CCC	TCC	TTC	GAG	GAG	AGT	GTG	GAG	CAG	TTC	ATC	CGC	CGC	670
Gly	Ala	Met	Pro	Ser	Phe	Glu	Glu	Ser	Val	Glu	Gln	Phe	Ile	Arg	Arg	
	210					215				220						
AAC	CTG	GGC	GAT	GAG	GTG	TTC	TTC	CGC	CTG	ATC	GAG	CCC	TTC	TGC	TCC	718
Asn	Leu	Gly	Asp	Glu	Val	Phe	Phe	Arg	Leu	Ile	Glu	Pro	Phe	Cys	Ser	
	225					230				235						
GGC	GTG	TAC	GCG	GGC	GAC	CCC	TCC	AAG	CTG	TCC	ATG	AAG	GCG	GCC	TTC	766
Gly	Val	Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	
240					245				250					255		
AAC	AGG	ATC	TGG	ATT	CTG	GAG	AAG	AAC	GGC	GGC	AGC	CTG	GTG	GGA	GGT	814
Asn	Arg	Ile	Trp	Ile	Leu	Glu	Lys	Asn	Gly	Gly	Ser	Leu	Val	Gly	Gly	
			260					265						270		
GCC	ATC	AAG	CTG	TTC	CAG	GAA	CGC	CAG	TCC	AAC	CCG	GCC	CCG	CCG	CGG	862
Ala	Ile	Lys	Leu	Phe	Gln	Glu	Arg	Gln	Ser	Asn	Pro	Ala	Pro	Pro	Arg	
		275					280					285				
GAC	CCG	CGC	CTG	CCG	CCC	AAG	CCC	AAG	GGC	CAG	ACG	GTG	GGC	TCG	TTC	910
Asp	Pro	Arg	Leu	Pro	Pro	Lys	Pro	Lys	Gly	Gln	Thr	Val	Gly	Ser	Phe	
		290					295					300				

CGC	AAG	GGC	CTG	AAG	ATG	CTG	CCG	GAC	GCC	ATT	GAG	CGC	AAC	ATC	CCC	958
Arg	Lys	Gly	Leu	Lys	Met	Leu	Pro	Asp	Ala	Ile	Glu	Arg	Asn	Ile	Pro	
305			310			315										
GAC	AAG	ATC	CGC	GTG	AAC	TGG	AAG	CTG	GTG	TCT	CTG	GGC	CGC	GAG	GCG	1006
Asp	Lys	Ile	Arg	Val	Asn	Trp	Lys	Leu	Val	Ser	Leu	Gly	Arg	Glu	Ala	
320			325			330			335							
GAC	GGG	CGG	TAC	GGG	CTG	GTG	TAC	GAC	ACG	CCC	GAG	GGC	CGT	GTC	AAG	1054
Asp	Gly	Arg	Tyr	Gly	Leu	Val	Tyr	Asp	Thr	Pro	Glu	Gly	Arg	Val	Lys	
340			345			350										
GTG	TTT	GCC	CGC	GCC	GTG	GCT	CTG	ACC	GCG	CCC	AGC	TAC	GTG	GTG	GCG	1102
Val	Phe	Ala	Arg	Ala	Val	Ala	Leu	Thr	Ala	Pro	Ser	Tyr	Val	Val	Ala	
355			360			365										
GAC	CTG	GTC	AAG	GAG	CAG	GCG	CCC	GCC	GCC	GCC	GAG	GCC	CTG	GGC	TCC	1150
Asp	Leu	Val	Lys	Glu	Gln	Ala	Pro	Ala	Ala	Ala	Glu	Ala	Leu	Gly	Ser	
370			375			380										
TTC	GAC	TAC	CCG	CCG	GTG	GGC	GCC	GTG	ACG	CTG	TCG	TAC	CCG	CTG	AGC	1198
Phe	Asp	Tyr	Pro	Pro	Val	Gly	Ala	Val	Thr	Leu	Ser	Tyr	Pro	Leu	Ser	
385			390			395										
GCC	GTG	CGG	GAG	GAG	CGC	AAG	GCC	TCG	GAC	GGG	TCC	GTG	CCG	GGC	TTC	1246
Ala	Val	Arg	Glu	Glu	Arg	Lys	Ala	Ser	Asp	Gly	Ser	Val	Pro	Gly	Phe	
400			405			410			415							
GGT	CAG	CTG	CAC	CCG	CGC	ACG	CAG	GGC	ATC	ACC	ACT	CTG	GGC	ACC	ATC	1294
Gly	Gln	Leu	His	Pro	Arg	Thr	Gln	Gly	Ile	Thr	Thr	Leu	Gly	Thr	Ile	
420			425			430										
TAC	AGC	TCC	AGC	CTG	TTC	CCC	GGC	CGC	GCG	CCC	GAG	GGC	CAC	ATG	CTG	1342
Tyr	Ser	Ser	Ser	Leu	Phe	Pro	Gly	Arg	Ala	Pro	Glu	Gly	His	Met	Leu	
435			440			445										
CTG	CTC	AAC	TAC	ATC	GGC	GGC	ACC	ACC	AAC	CGC	GGC	ATC	GTC	AAC	CAG	1390
Leu	Leu	Asn	Tyr	Ile	Gly	Gly	Thr	Thr	Asn	Arg	Gly	Ile	Val	Asn	Gln	
450			455			460										
ACC	ACC	GAG	CAG	CTG	GTG	GAG	CAG	GTG	GAC	AAG	GAC	CTG	CGC	AAC	ATG	1438
Thr	Thr	Glu	Gln	Leu	Val	Glu	Gln	Val	Asp	Lys	Asp	Leu	Arg	Asn	Met	
465			470			475										
GTC	ATC	AAG	CCC	GAC	GCG	CCC	AAG	CCC	CGT	GTG	GTG	GGC	GTG	CGC	GTG	1486
Val	Ile	Lys	Pro	Asp	Ala	Pro	Lys	Pro	Arg	Val	Val	Gly	Val	Arg	Val	
480			485			490			495							
TGG	CCG	CGC	GCC	ATC	CCG	CAG	TTC	AAC	CTG	GGC	CAC	CTG	GAG	CAG	CTG	1534
Trp	Pro	Arg	Ala	Ile	Pro	Gln	Phe	Asn	Leu	Gly	His	Leu	Glu	Gln	Leu	
500			505			510										
GAC	AAG	GCG	CGC	AAG	GCG	CTG	GAC	GCG	GCG	GGG	CTG	CAG	GGC	GTG	CAC	1582
Asp	Lys	Ala	Arg	Lys	Ala	Leu	Asp	Ala	Ala	Gly	Leu	Gln	Gly	Val	His	

	515	520	525	
CTG GGG GGC AAC TAC GTC AGC GGT GTG GCC CTG GGC AAG GTG GTG GAG				1630
Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Lys Val Val Glu				
	530	535	540	
CAC GGC TAC GAG TCC GCA GCC AAC CTG GCC AAG AGC GTG TCC AAG GCC				1678
His Gly Tyr Glu Ser Ala Ala Asn Leu Ala Lys Ser Val Ser Lys Ala				
	545	550	555	
GCA GTC AAG GCC TAA GCGGCTGCAG CAGTAGCAGC AGCAGCATCG GGCTGTAGCT				1733
Ala Val Lys Ala				
	560	563		
GGTAAATGCC GCAGTGGCAC CGGCAGCAGC AATTGGCAAG CACTTGGGGC AAGCGGAGTG				1793
GAGGCGAGGG GGGGGCTACC ATTGGCGCTT GCTGGGATGT GTAGT				1838

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 <213> Artificial Sequence

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 <223> Designed oligonucleotide primer used for amplifying a DNA fragment containing a *Chlamydomonas reinhardtii*-derived PPO gene

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